

Understanding how contact heterogeneity alters epidemic outcomes is central to evidence-based preparedness. Classical Introduction High-resolution contact studies routinely report heavy-tailed degree distributions with a small fraction of Motivated by this gap, we address the following research question: **How does introducing degree heterogeneity** This investigation contributes three insights. (i) The network reproduction number depends linearly on the mean excess Methodology Network Construction Two static undirected networks of identical order $N = 5,000$ were generated using SEIR Model on Networks Each node can occupy one of four compartments: Susceptible (S), Exposed (E), Infectious (I) $E\sigma I$, $I\gamma R$. Ten randomly chosen nodes were seeded as infectious; all others were susceptible at $t = 0$. The choice maintains identity Deterministic Threshold Analysis Under homogeneous-mixing the next-generation approach gives $\mathcal{R}_0^{HM} = \beta/\gamma$. For a

Thus the epidemic threshold in terms of β is $\beta_c^{net} = \gamma/q$. Substituting the empirical moments we obtain $\beta_c^{ER} = 0.014$ and $\beta_c^{BA} = 0.006$. Stochastic Simulation Protocol We used **fastgemf** version 0.4.2 to run exact continuous-time simulations. For each network we Results Analytical Threshold Comparison Table summarises critical ratios. BA heterogeneity lowers β_c by a factor of 2.3.

	Topology	$\langle k \rangle$	$\langle k^2 \rangle$	β_c ($\gamma = 1/7$)
[ht] Deterministic epidemic thresholds	Homogeneous	—	—	0.143
	ER	7.98	71.5	0.014
	BA	7.99	167.2	0.006

Stochastic Metrics at $\beta = 0.05$ Twenty-run averages are displayed in Table . Degree heterogeneity elevates I_{\max} by 23% and R_{\max} by 6%. Network

[ht] Average epidemic metrics over 20 stochastic realisations ($\beta = 0.05$). Standard deviations in parentheses. ER 6.1 (0.4) BA 7.9 (0.5)

Representative average trajectories are plotted in Figure . The BA curve exhibits a steeper ascent and decay, indicative of a higher peak and faster return to baseline. [http://www.osti.gov/servlets/handle/11366/46700] [width=0.48]results_avg_BA.png [width=0.48]results_avg_ER.png Average exposed (E) and infectious (I) prevalence for Sensitivity to Transmission Rate Increasing β from 0.03 to 0.08 monotonically amplifies peak size and reduces time-to-peak. Discussion Our findings reinforce and extend prior insights on the pivotal role of degree variance in epidemic propagation. From a methodological standpoint, the contrast between analytic thresholds and stochastic metrics highlights complementary perspectives. Limitations include the use of synthetic networks without clustering, absence of demographic turnover, and equal per-capita rates. Conclusion Degree heterogeneity profoundly alters SEIR epidemic dynamics. Analytical derivations show that the basic reproduction number is $\mathcal{R}_0 = \beta/\gamma$. *References 9

R. Pastor-Satorras and A. Vespignani, “Epidemic spreading in scale-free networks,” *Phys. Rev. Lett.*, vol. 86, no. 14, pp. 3096–3099, 2001.
M. Boguñá, R. Pastor-Satorras, and A. Vespignani, “Absence of epidemic threshold in scale-free networks with degree correlations,” *Phys. Rev. Lett.*, vol. 87, no. 23, pp. 236101, 2001.
V. M. Eguíluz and K. Klemm, “Epidemic threshold in structured scale-free networks,” *Phys. Rev. Lett.*, vol. 89, p. 108701, 2002.
L. Muchnik, S. Pei, L. Parra, S. Sreenivasan, J. Sredner, and H. Makse, “Origins of power-law degree distribution in the human contact network,” *Phys. Rev. Lett.*, vol. 90, p. 018701, 2003.
H. Kang, M. Sun, Y. Yu, and X. Zhang, “Spreading dynamics of an SEIR model with delay on scale-free networks,” *IEEE Transactions on Network Science and Engineering*, vol. 1, no. 1, pp. 1–11, 2014.
Reproducibility Materials All Python scripts, network files and CSV outputs are available in the accompanying output directory.